

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 30, 2002, 16:02:56 ; Search time 70.14 Seconds
(without alignments)
1061.057 Million cell updates/sec

Title: US-09-357-273a-2
Perfect score: 5139
Sequence: 1 MPARRLLLTLLLPGLGIF.....QPYFHEPPEPQPPVPDAL 977

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Archived: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR_68:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1749.5	34.0	983	2	hypothetical prote
2	1004	19.5	1115	2	protein kinase TRE
3	959.5	18.7	1072	2	serine threonine-p
4	655.5	12.8	393	2	probable protein k
5	334	6.5	1114	2	serine/threonine-s
6	312	6.1	1108	2	translatation initia
7	297.5	5.8	1077	2	hypothetical prote
8	295	5.7	1257	2	serine/threonine-s
9	294	5.7	741	2	2-5A-dependent kina
10	286.5	5.6	659	1	protein kinase byr
11	285.5	5.6	647	1	LIM protein kinase
12	283.5	5.5	647	1	LIM protein kinase
13	281	5.5	547	2	hypothetical prote
14	280.5	5.5	647	1	LIM protein kinase
15	280.5	5.5	1271	2	protein kinase
16	278.5	5.4	1230	2	probable serine/th
17	277.5	5.4	1230	2	serine/threonine p
18	275.5	5.4	1192	2	Ca2+/calmodulin-de
19	275	5.4	516	1	probable MAP kinas
20	275	5.4	594	2	serine/threonine-s
21	275	5.4	658	2	hypothetical prote
22	275	5.4	708	2	calcium-dependent
23	274.5	5.3	490	2	phosphorylase kina
24	274	5.3	406	1	phosphorylase kina
25	272	5.3	406	1	setum-inducible ki
26	272	5.3	682	2	hypothetical prote
27	268.5	5.2	1171	2	Ca2+/calmodulin-de
28	268.5	5.2	533	1	calmodulin-depende
29	268	5.2	509	2	B44442

30	268	5.2	530	2	D44412	Ca2+/calmodulin-de
31	267.5	5.2	495	1	S46284	calcium-dependent
32	267.5	5.2	608	2	T01833	serine/threonine-s
33	267	5.2	651	2	A96591	MEK1-related prote
34	266	5.2	479	2	B45771	2-5A-dependent RNA
35	265.5	5.2	478	1	S04365	Ca2+/calmodulin-de
36	264	5.1	575	2	C85059	probable calcium d
37	264	5.1	608	2	C96575	probable MEK kinas
38	263	5.1	542	2	T08777	probable protein k
39	262.5	5.1	912	2	A53215	protein kinase C (
40	261.5	5.1	733	2	A57459	ribosomal protein
41	261	5.1	603	3	A47545	protein kinase (EC
42	260.5	5.1	387	1	K1RBRG	phosphorylase kina
43	259.5	5.0	478	1	A30355	Ca2+/calmodulin-de
44	259.5	5.0	560	2	S51600	phosphorylase kina
45	259	5.0	603	2	S34130	serine/threonine-s

ALIGNMENTS

RESULT 1	19874	hypothetical protein C41C4.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans		
C:Date: 15-Oct-1999	#sequence_revision 15-Oct-1999	#text_change 15-Oct-1999
C:Accession: T19874		
R:Burton, J.		
A:Submitted to the EMBL Data Library, February 1995		
A:Reference number: Z19190		
A:Accession: T19874		
A:Status: preliminary; translated from GB/EMBL/DBJ		
A:Molecule type: DNA		
A:Residues: 1-983 <WILL>		
A:Cross-references: EMBL:Z48045; PIDN:CAA8100.1; GSPDB:GNO0020; CESP:C41C4.4		
A:Experimental source: clone C41C4		
C:Genetics:		
A:Gene: CESP:C41C4.4		
A:Map position: 2		
A:Introns: 29/3; 71/1; 242/1; 283/3; 392/1; 763/1; 901/3; 926/3		
Query Match	34.0%; Score 1749.5; DB 2; Length 983;	
Best local similarity	38.5%; Pred. No. 5.9e-73;	
Matches 395; Conservative 167; Mismatches 285; Indels 179; Gaps 26;		
QY 6 LLLLTLLLPGLGIFGSGTVLP-----ETLFFVSLDGLAAVSKRT 49		
DB 7 LFTFFLL-----FSSVICISTPGFRNDHESIGDDEKTSITLVSTIDGRALDSET 61		
QY 50 GSIRKTLKEDPYLVPTVNEEP-ALLPDPNGSLTLGSKNNEGTLKLPFTIPELVQASP 108		
DB 62 GKIKWTLDEEPLRSPSAVQKGFELPNPLDGLYL--KNSSIKKLFPNLPQLVHASP 118		
QY 109 CSSSGGILYMGKKDIDWYIDLTLGEEK-----OOTLSSAFADSICPST- 151		
DB 119 CKNNGGILYAGSKRDVWGIDPKTGLKVEYILLNLSDKILFLQVETLSSASADRCPANQ 178		
QY 152 :SLLYLGRTEYITMYDKTRRLRNATYFDYAASLPDEGDKMSHFVNSGDLVTVTD 210		
DB 179 KOTILFGRTEYIVSMFDEKRNKGTWNATFNDSAHLLPEVNMWPKHVAASSHGIIIFPD 238		
QY 211 SSSGCVLWQNASPVAVFYVQREGELKRVMIINAVETLRLTMTSGEVGKITWKPKPF 270		
DB 239 RFTGEMRWDOKQPVVALYLLRDGLRLKLPDEVMGKTEMEN--VANNIFVDDWPIYVL 295		
QY 271 -----PKTEAKSKLFTPLIVYKSTSLYASPSMW-HEGVAVVPRGSTLPLEGPOTDG 323		
DB 296 GYNADPQTTSLTNQFPALFVGESSFGIYATEALVDHQTITYSKLLGLPRLBEPAPIA 355		
QY 324 VTIGKGEVCV-----TPSTVDYKDPGLGSKSNKLNLYLRNWLIGHHETP-LSAST 373		
DB 356 LTEMKEEYLPRRPRIIRNIPPSITHKTSDG-----EYLLGIGHYRPMATWAT 403		

QY 374 KMLEPSENNLPKHNRENVIPADSEKKSPFEVINVLVQTSNAPTTYSRDVEKRAHPARP 433
Db 404 ILPTRP-----VPCPK-----AIGSTTERPPOLGPE-----PQK 438
QY 434 E-----APDMSLMDATILSTFLLIGWAFITTPPLSMHQOOLQHQFOQ 480
Db 439 EDTSFILLNNHPRIPTYALTVMFALLTVIMQCG-----RQMDQCKST 483
QY 481 KELEKIDLOLQOQOQLPFHPGDTAQQGELDDTSCPTPSSSTSSPTSPRASNHSLSG 540
Db 484 SRMDSEFIVN-----PGE-----SHSAQTSKOS-----507
QY 541 SSASKAGSSPSLEDDDEETRSVIYVGIKISFCPKDVLGHGAGTIIYRGAFDNRYAVKR 600
Db 508 NRSFGFNANKIETPEG-----WMAVGSKLMTSPSILGTCGEGTYVYRGTFDGRYAVKR 563
QY 601 ILPECSFADREVOLLRESDEHPVIRYFCTEKROFOYIAIELCAATLOEYVEOKDFAH 660
Db 564 VSEFVFAHREADLRESDPNPHVIRYFCMESDSQFRLALELCLASINDYVEOKVOQ 623
QY 661 ---LGLPITLLQOTSGALHLHSINTYHRODKPHNILLMSNANHKIKAMISDFGLCKR 717
Db 624 NVTIALMDI--MKATGGLAHLHASKIVHRODKPQNVLLTMSAQREMAVVISDFGLCKR 681
QY 718 LAVGRHSFSR--RSGVDTGEGMIAPEMLSEDCKENPTYVDVDFISAGCVYVYVSEGSHP 775
Db 682 VQPGKNSISGSIAGSLAGTQDMIAPEVL---ISASTSYVDVDFISLGCITFYVLTSGHP 738
QY 776 GKSQROANTLLGACSLDCLPHEKEDVIARELKMIAMDPOKPSANDVLKHPFWSL 835
Db 739 GKSLHROANTVNGEYTLNKL-ADLDMDSLADLLISMLNVEPLHRLTADAVLNHPFWTS 797
QY 836 EKQLQFQDVSDRIKESLSQRIYKQLRGGRVAVKMMQRENTDPLQDRLKFRYKKG 895
Db 798 EKRLAIFSDVSDRKEKEDNSPVVARIETDARIYVCGGRKXICDLAKEDLRKFRYKSF 857
QY 896 SVYDILLRANKKKHHYRELPAVEVETLGLPDDFCYFSRPHLLAHYIRAMELCSHER 955
Db 858 SVYDILLRANKKKHHYRELPAVEVETLGLPDDFCYFSRPHLLAHYIRAMELCSHER 917
QY 956 LFQPPY 961
Db 918 VFRRY 923

RESULT 2
A47541
protein kinase IRE1 (EC 2.7.1.-) precursor - yeast (*Saccharomyces cerevisiae*)
N.Alternate names: BIP-need-sensing protein kinase ERN1, protein YHR079C
Species: *Saccharomyces cerevisiae*
Date: 03-May-1994 #sequence,revision 03-May-1994 #text_change 23-Mar-2001
Accession: A47541, S46816, S22629
R.Mori, K.; Ma, W.; Gething, M.J.; Sambrook, J.
Cell 74, 743-756, 1993
A:Title: A transmembrane protein with a cdc2(+)/CDC28-related kinase activity is required for cell growth in *S. cerevisiae*
A:Reference number: A47541; MUID:53364990
A:Accession: A47541
A:Molecule type: DNA
A:Residues: 1-1115 <MOR>
A:Cross-references: GB:119640; NID:g3933280; PIDN:AAA34489.1; PID:g3933281
R.Favell, T.
submitted to the EMBL Data Library, June 1994
A:Description: The sequence of *S. cerevisiae* com1d 9205.
A:Reference number: S46795
A:Accession: S46816
A:Molecule type: DNA
A:Residues: 8-1115 <FAV>
A:Cross-references: EMBL:U10556; NID:g500825; PIDN:AAB68894.1; PID:g500837; MIPS:YHR079C
R.Nikawa, J.I.; Yamashita, S.
Mol. Microbiol. 6, 1441-1446, 1992
A:Title: IRE1 encodes a putative protein kinase containing a membrane-spanning domain and a

[illegible]

Query Match 12.8%; Score 655.5; DB 2; Length 393;
Best Local Similarity 34.9%; Pred. No. 2.4e-23;
Matches 140; Conservative 77; Mismatches 149; Indels 35; Gaps 9;

566 VKISFCRDKVGHGAETIYIRGFMFNDVAVKRIIEPCECSFADREVOQLRESEHENV 625
18 IGLKFLSKKEI-AKGSNGTVFEGIEGRPAVKRLVRSHEHVAKEKIONLONLDOHNTI 76
626 IRYFCTEKROFOYIAELCAATLOEYEOKDFALHLEPITLLQOTTSGLAHLISLNIY 685
77 IRWGEVLEDOOPVILSERCTCSLDLI--KYLEFSTKTVLENDSTEG----- 124
686 HRDLKPNHILISMPNAHGKIKAMISDFGLCKLAVGRHSFSRSGVPTGEGNIABEMLSE 745
125 -----PQVVLISKDMT---LSAKLSDMGISKRMSRDMSSLGLHANGSSSGQAPAEQLLQ 176
746.DCKENPTTVDFISAGCVFYVYVSGSHPRFGKSLQORANILLAGCSLDCLH--PEKHEDV 803
177 G---RQTRAVDMFSLGCVIFYTITGCKHPFGDLERDVNIYVKNKVDLVEHVP----- 228
804 IARELEKIMADPOKRSANDVLKHPFWSLEKQLOFPOVSDRIEKES--LDGPYKQ 861
229 -ASDLISRLNPDPLRSATEVLLHPMFWSSEMRSLFLRDSQVLEENREADESELKA 287
862 LERGRAVVKMDRENITDPLQTLRKFRYKGGSVRDLLRAMRKKHNYRELPAVEBET 921
288 MESTAPVAIGCKWDEKLEPVFTINGRYRKYDSIRDLRYIRKKNHRLPREIDEL 347
922 LGTLPDDFVCYFTSRFPPLHANTYRAMEL-CSHERLQOPY 961
348 VGTVEGEDEFYFAVRFPKLLIEVYRVLISLHCRREEVFRKYF 388

RESULT 5
T14351
serine/threonine-specific protein kinase (EC 2.7.1.-) PERK, ER-resident - mouse
N:Alternate names: translation initiation factor eIF-2 alpha chain kinase
C:Species: Mus musculus (house mouse)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T14351
R:Harding, H.P.; Zhang, Y.; Ron, D.
Nature 397, 271-274, 1999
A:Title: Translation and protein folding are coupled by an endoplasmic reticulum resident
A:Reference number: Z18000; MUID:99127894
A:Accession: T14351
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1114 <HAR>
A:Cross-references: EMBL:AF076681; NID:94107512; PID:94107513; PIDN:AAD03337.1
A:Experimental source: Strain Swiss-3T3-NIH
A:Function:
Description: PERK is implicated in a signalling pathway that attenuates protein translocation.
C:Keywords: phosphotransferase

Query Match 6.5%; Score 334; DB 2; Length 1114;
Best Local Similarity 18.6%; Pred. No. 4.3e-08;
Matches 210; Conservative 191; Mismatches 375; Indels 356; Gaps 50;

2 PARALLLTLTLLPLGL-----IFG-----STSY 26
7 PGRALLLTLTLLGLCAAGISAVAPARSLAPASETVFGLGAAPASARPAVATAEV 66
27 TL-----PE-----TLFVSTLDSLHAY-SKRTGSIKMTL 56
67 TVEDEALPAAAGEPESATERPDDVELRPRGRSLVITSLDGRALALDAENDGKKQMDL 126
57 KEDPVLQVPTHVEEPALPD-----PN-DGSLYTLGSKNNEGLTKLPPTIPELVQASPCRS 111
127 DVGSGSLVSSSLSKREYVGNKMIITSLDGDLFQ-WDRDRESMEANVPFYTESLLESS-YKF 184
112 SDGIYMKKODIYVIDLTLGEKOOTLSSAF-----ADSLCPSTSLYLGRTETITM 165

185 GDDVVLVGKSLITYGLSAYSG-KLRYTCSALGCRWMSDEMEEDLTLQOTKTVRA 243
166 YDTRRELRLWN-----ATYEDYAAALPEDEGDKMSHFVSN----- 201
244 VGRSGSKKNFVSVGHFELRYIPMETRAGFLIESFFKGGKNEKDSKIISDVEDEQATMLD 303
202 -----GDGLVTVDSSEGDVLIQNYASPVAVYVWQREGRLKRVMIINAVETLRYLT 254
304 TVIKVSVADMVMAFSRRGRLMEYQCTPLASAML-VRDG--KVIPISLFDLT----- 355
255 FMSGVEGATKKKYPFRET-----EAKSKITPLLYGKYSTSLYASPSM----- 299
356 -----SYASEEALDEEDIVEAARGATENSIVYLGMRGQLYLOSSRVYSEKF 403
300 -----VHEGVAVVVRGSR--PLLEGPOTDGVTG--DKGECVITPS-TVQKFPDG 345
404 PTPSKALESVNGENAIITPLTKMKPLHSPSRPTVYVLSDEFDKLSNDKYSHEEYING 463
346 LSKRKNLYLRNYWLLIGHETPLSASTKMLERFPNNLPKHRENYIPADS-----EKS 399
464 ALSILOVRYDNGYVLPYKREBN-KRSTQIVRYFLDS-PhysknirKDPILLHMKEI 521
400 FEEVINLVDOISENAPTVSRV-----EKPANARAPAPVDSMLKDMATILSTF 452
522 FGTILLICVAT-----TVIRLFHPDRKRESETOCQTESKYDSVADVSDNSMDM 576
453 LLIGVAFVIT-----YPL-----SM 468
577 KYSGVSRVLDPEFIEQCMGRGFGVFEAKNKVDDCAVYAIKRIPLRRELAREKVMREV 636
469 HQOQOOLH-----GQFOKELEKIQLQOQOOLPFRPG----- 502
637 KALKLEHGIIVRYPNAMLETTPREKOEEMEI-WLKDESTDWPLSPSPMDAPSVKIRR 695
503 -DTADGELDIDSGPYSSS-----GTSPTSPPASNHSICS-----GSSASAGSSP 550
666 MDPSTKQIOEIVAPSPRSRFSVIGSCGOTSSSESQSPLESFSGTDCGSDSADANAY 755
551 SLEOD-----DGEETSVIVGKISFCPKVILGH-----GAEGTIYV----- 587
756 NIQDSCILNDCEDVEDGYDGNDEGH-----SPELCPSASPTRETSSTIVEEDSGC 810
588 -----RG--MFDNDVAVKRIILPECFSF-ADREVOQLRESEHNP-----NVI 626
811 GNASSKEPRGNRLHDGHHYVKKLTLDCSSSRSSSEATTLSTPTRTTSLDPTKMTV 870
627 RYFCTEKROFOYIAELC-AATLOEYEOKDFALHLEP-----ITLLQOTTSGLAHL 679
871 GOLPSSRPVYLYIOMOLCKRENLDMMNR-----CSLEDRHGVCILFIQIAEAVEFL 926
927 HSKGLMHRLDKRNSIFFTMDV-----VKVGDGFLVTAMDODEEQVLTLPAPAVATHTG 981
731 VPGTEGWIAPKLESDCKENPTTVDFISAGCVFYVYVSGSHPRFGKSLQORANILLAGC 790
982 QVGTGTLVSPEDIRHN-----NSHKVDIFSGLILPELL-----YPESTOMER-VRLTIVR 1033
791 SLDC-----LHPEKHEVDIARELEKMIAMPORPSANDVLKHPFWSLE 836
1034 NIKFPLLTQKYPQEH-----MAYQDMLSPSTREPTATDIENAVIENLE 1079

RESULT 6
T17455
translation initiation factor eIF-2 alpha chain kinase (EC 2.7.1.-) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Mar-2000
C:Accession: T17455
R:Shih, Y.; Valtem, K.M.; Sood, R.; An, J.; Liang, J.; Stramm, L.E.; Wek, R.C.
Mol. Cell. Biol. 18, 7499-7509, 1998
A:Title: Identification and characterization of pancreatic eukaryotic initiation factor